B1 cont'd

plant cells and specific tissues. The methods involve modulation of the levels of enzymes in the galactomannan biosynthetic pathway. The synthesis of the gum galactomannan is catalyzed by the enzymes mannan synthase and galactosyl transferase, from the substrates GDP-mannose and UDP-galactose. The formation of the substrate GDP-mannose, from mannose-1-phosphate and GTP, is catalyzed by the enzyme GDP-mannose pyrophosphorylase.

Please replace the paragraph beginning on page 5, line 17, with the following rewritten paragraph:

--The present invention is further drawn to compositions and methods for manipulating the levels of enzymes of the galactomannan biosynthetic pathway in plants, plant cells, and specific plant tissues. By enzymes of the galactomannan biosynthetic pathway is meant GDP-mannose pyrophosphorylase, mannan synthase and galactosyl transferase. It is recognized that as the galactomannan pathway is further elucidated, newly discovered galactomannan biosynthetic enzymes are included in the methods of the invention. Compositions are nucleic acids relating to genes encoding enzymes of the galactomannan biosynthetic pathway in plants, preferably to GDP-mannose pyrophosphorylase or GDP-mannose pyrophosphorylase-like genes. Preferably, the GDP-mannose pyrophosphorylase is native to maize or a leguminous plant. By native to maize or a leguminous plant is meant that the GDP-mannose pyrophosphorylase may be present in a naturally occurring or cultivated species of maize or a leguminous plant. Nucleotide sequences for a maize GDP-mannose pyrophosphorylase gene and the amino acid sequence for the GDP-mannose pyrophosphorylase protein encoded thereby are disclosed, as well as fragments and variants thereof. These sequences are set forth in SEQ ID NOS:1 and 2. The maize GDP-mannose pyrophophorylase sequences were disclosed in U.S. provisional application Serial No: 60/096,782, filed 17 August

B2

B2 cont'd

1998, to which the instant application claims priority and which is incorporated herein by reference. The sequences find use in the construction of expression vectors for subsequent transformation into plants of interest, as probes for the isolation of other GDP-mannose pyrophosphorylase-like genes, as molecular markers, and the like.

Please replace the paragraph beginning on page 18, line 18 with the following rewritten paragraph:

B3

A full-length cDNA sequence encoding maize GDP-mannose pyrophosphorylase gene was isolated from the maize genomic project. Maize root and culture cell cDNA libraries were constructed according to the manufacturer's instructions (Gibco-BRL). cDNA clones were partially sequenced from 5 -end. 5 -sequences of cDNA clones were then compared to the Saccharomyces cerevisiae V1G9 GDP-mannose pyrophosphorylase gene (Hashimoto et al., (1997) J. Biol. Chem. 272:16308-16314) with the BlastX subroutine. A clone that showed significant homology to the gene was sequenced completely. The nucleotide sequence and the deduced amino acid sequence are set forth in SEQ ID NOS:1 and 2, respectively. Gene sequences are cloned into a plasmid vector in the sense orientation so that they are under the transcriptional control of the ubiquitin promoter. A selectable marker gene may reside on this plasmid or may be introduced as part of a second plasmid. The transformation construct is then available for introduction into maize embryos by bombardment methods as described in Example 2.

In the claims:

Please cancel claims 15, 74 and 75 without prejudice.

Please amend claims 11, 56, 65, 66, and 73 as follows: